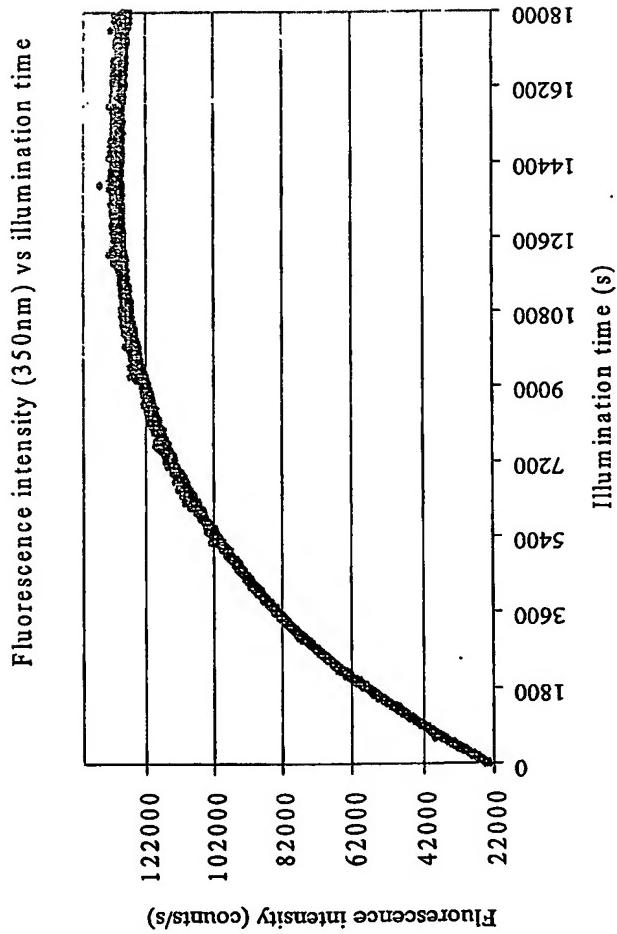
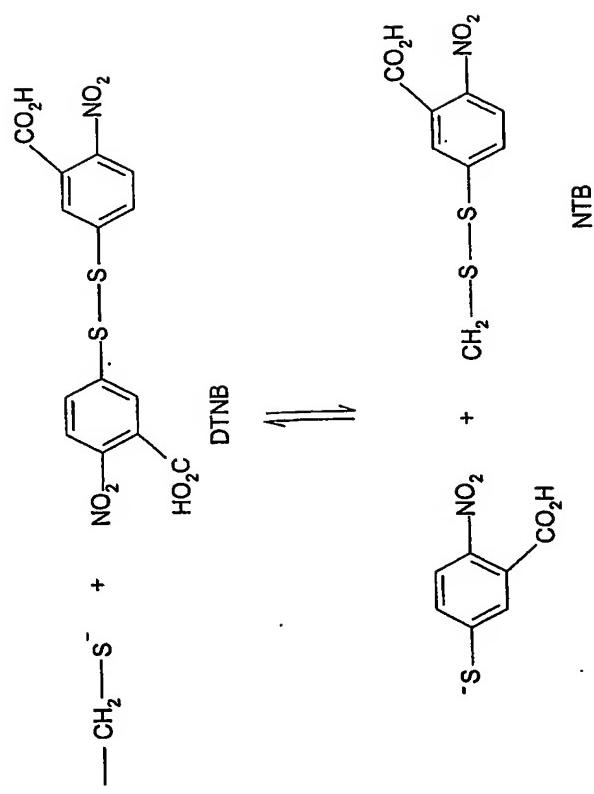


1/20

Figure 1

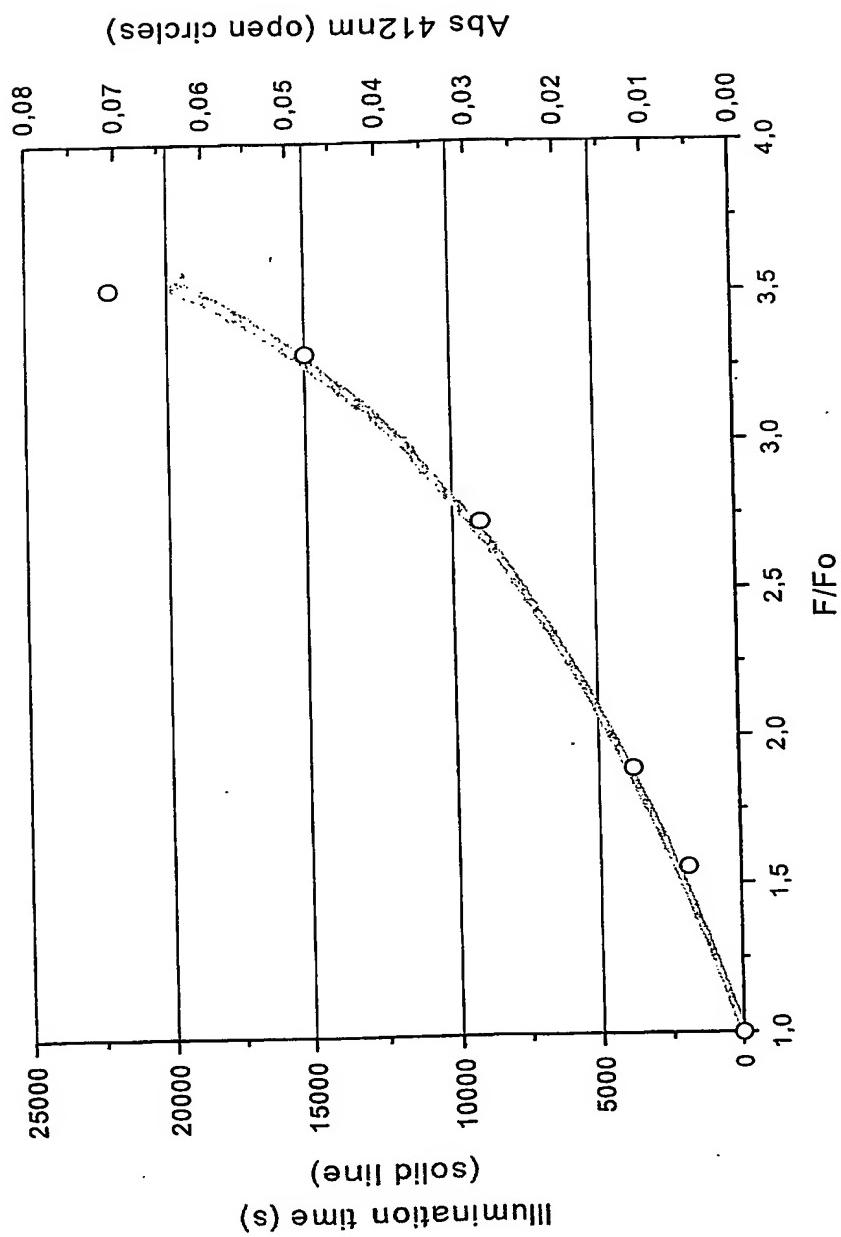
2/20

Figure 2



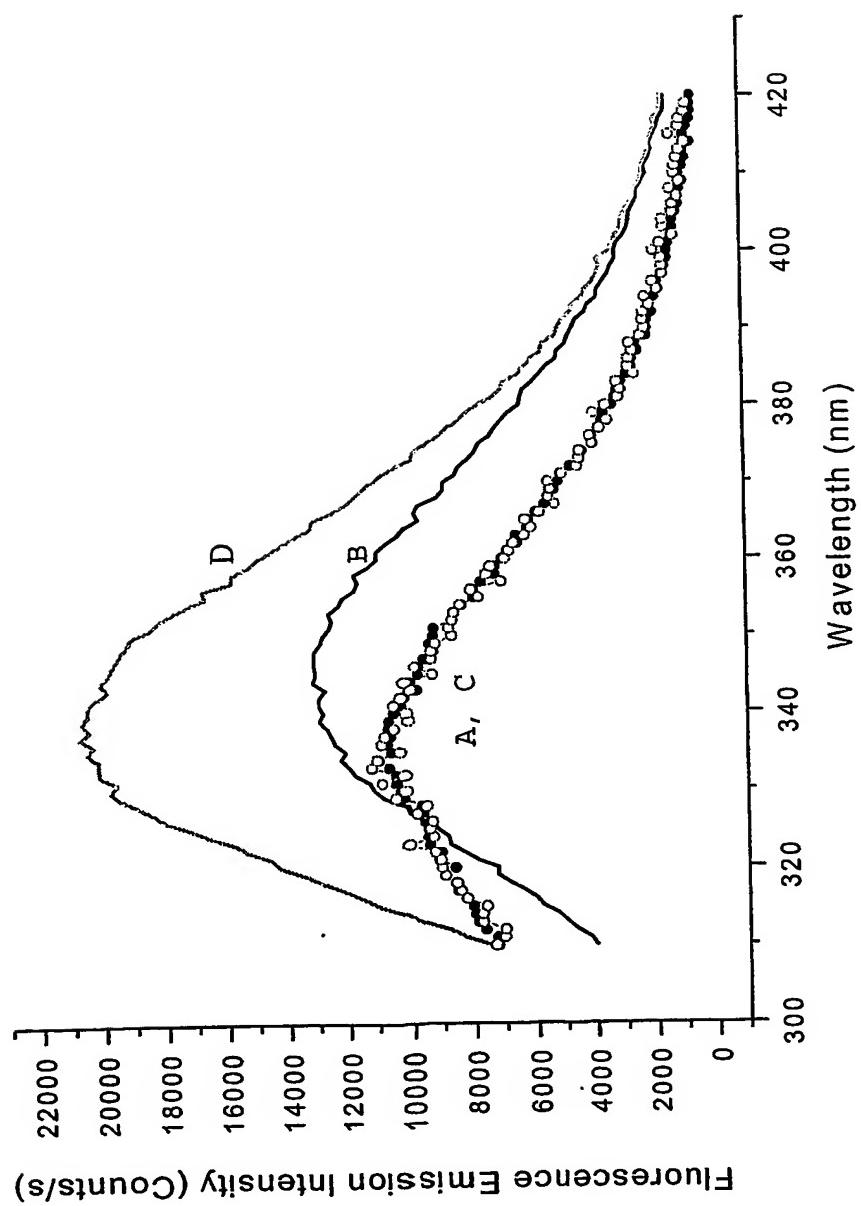
3/20

Figure 3



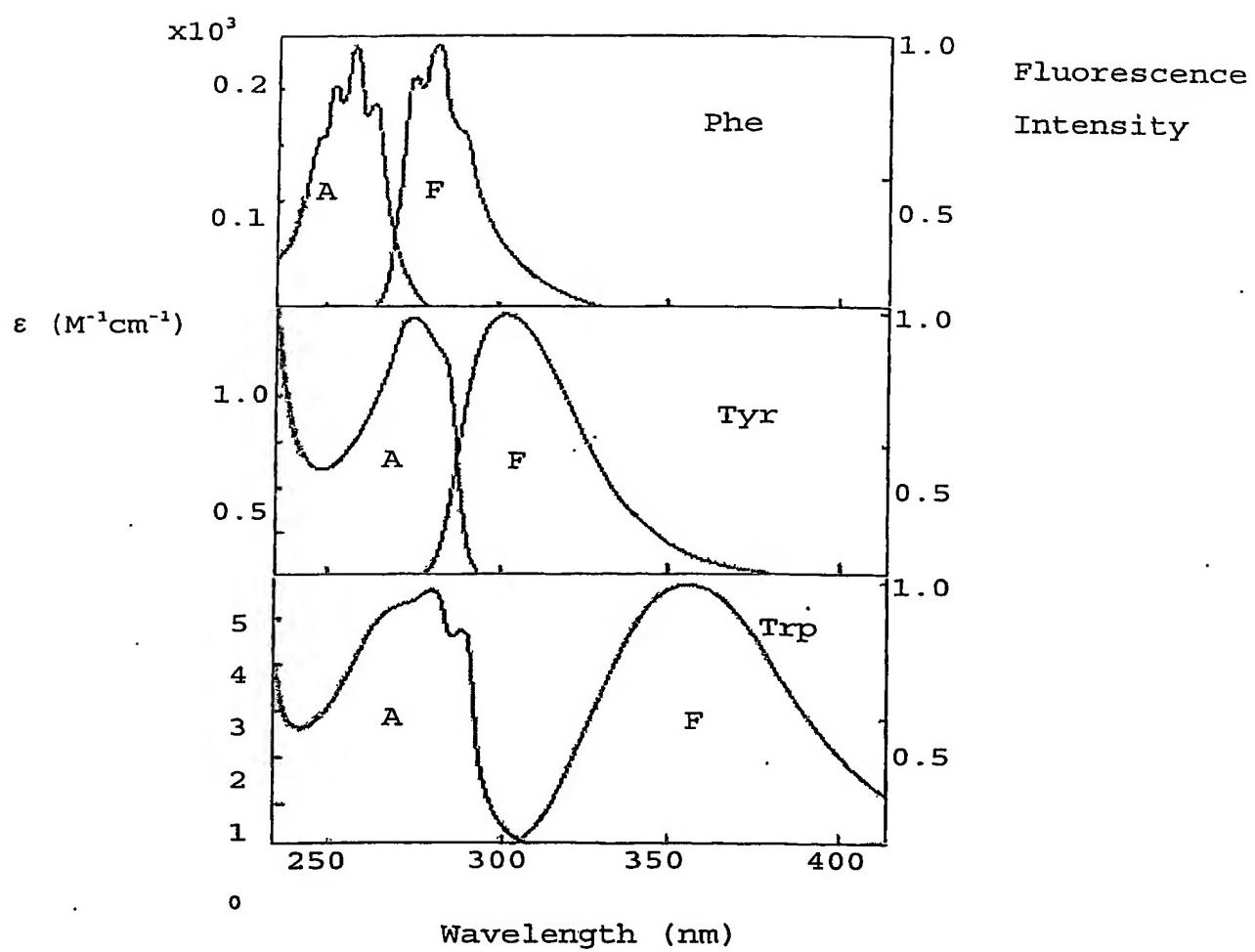
4/20

Figure 4



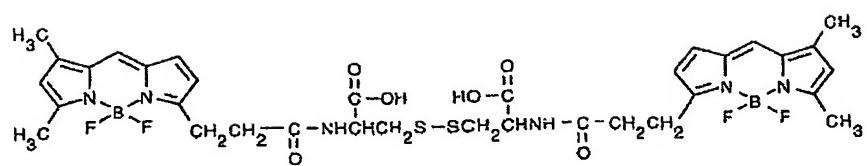
5/20

Figure 5



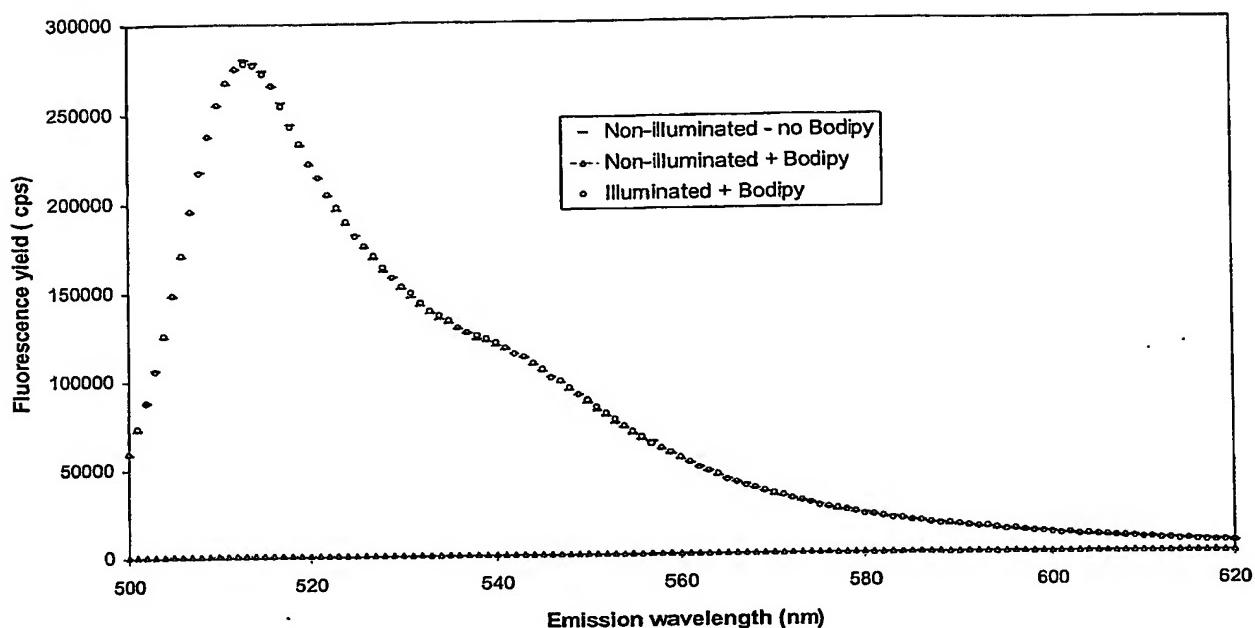
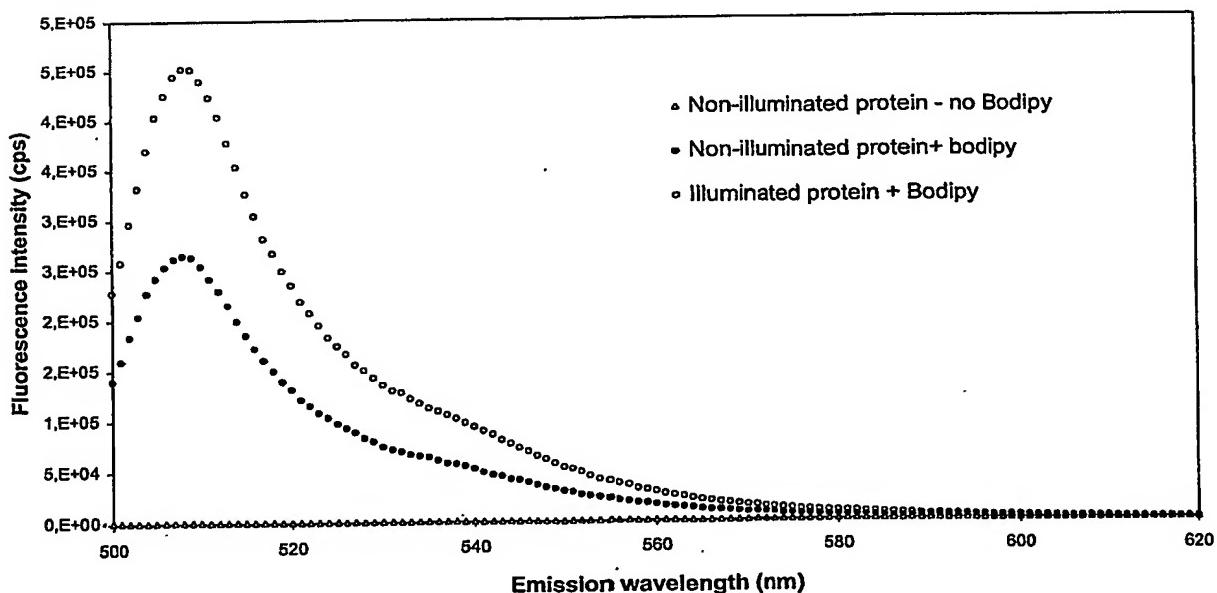
6/20

Figure 6



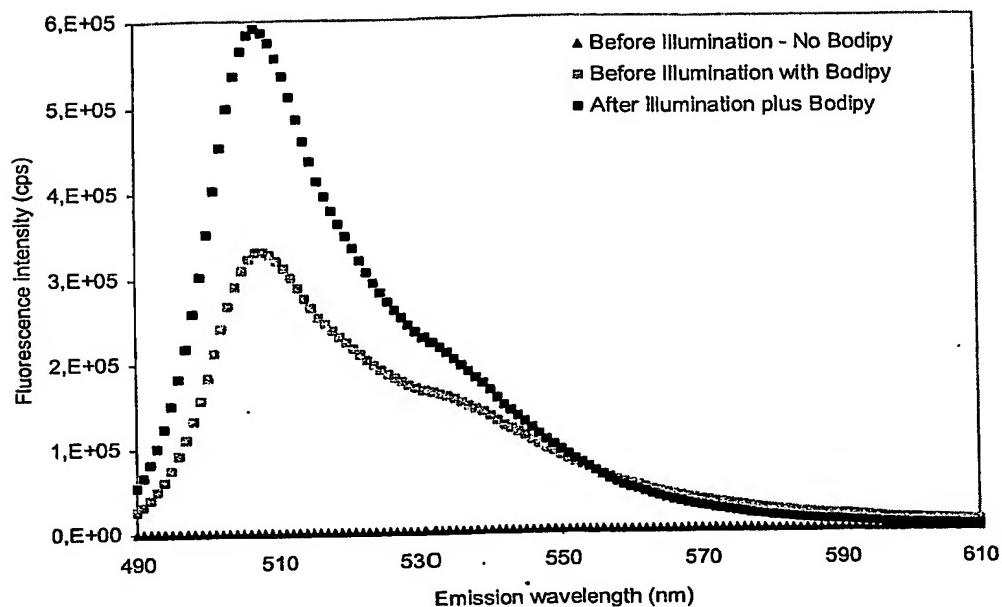
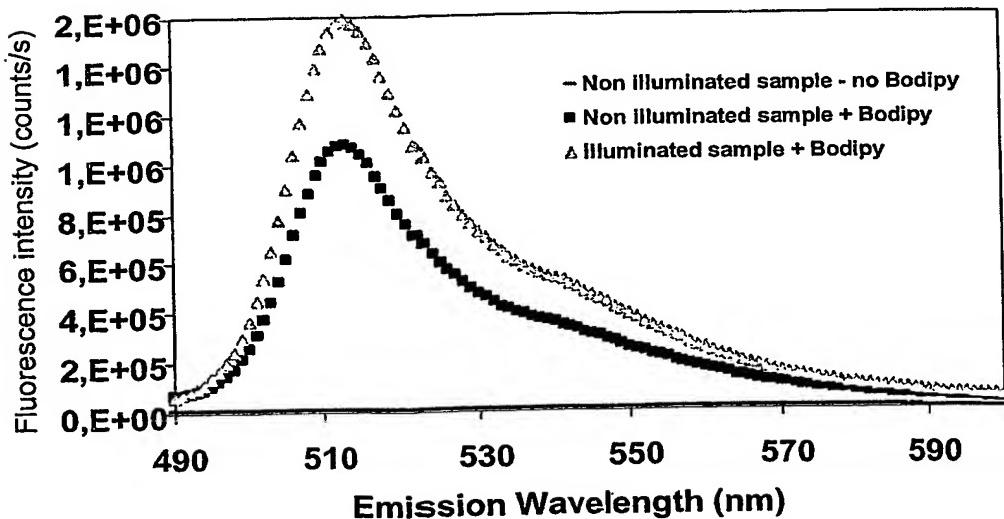
7/20

Figure 7

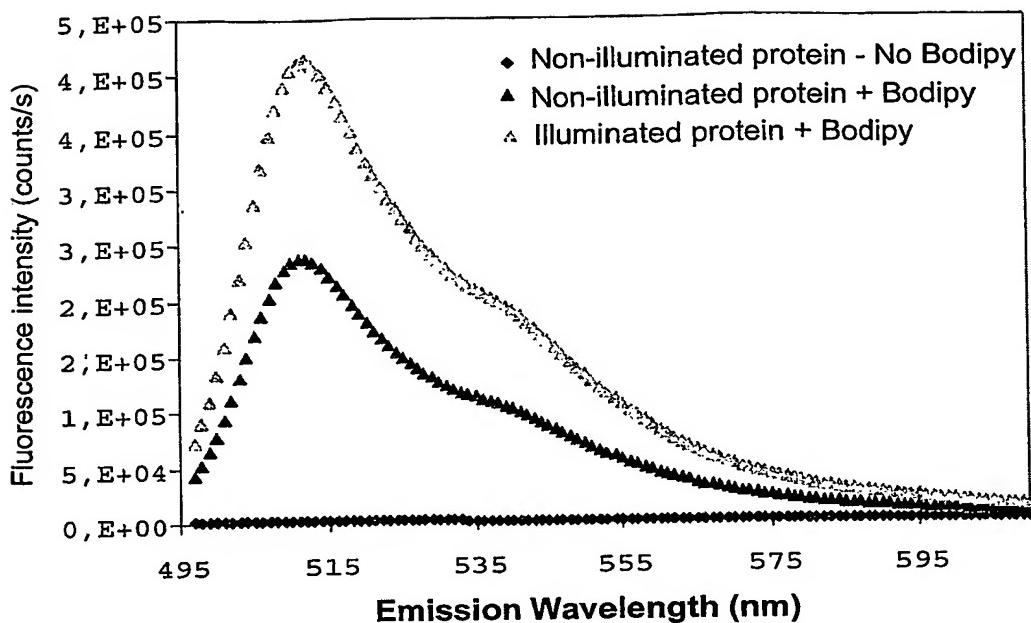
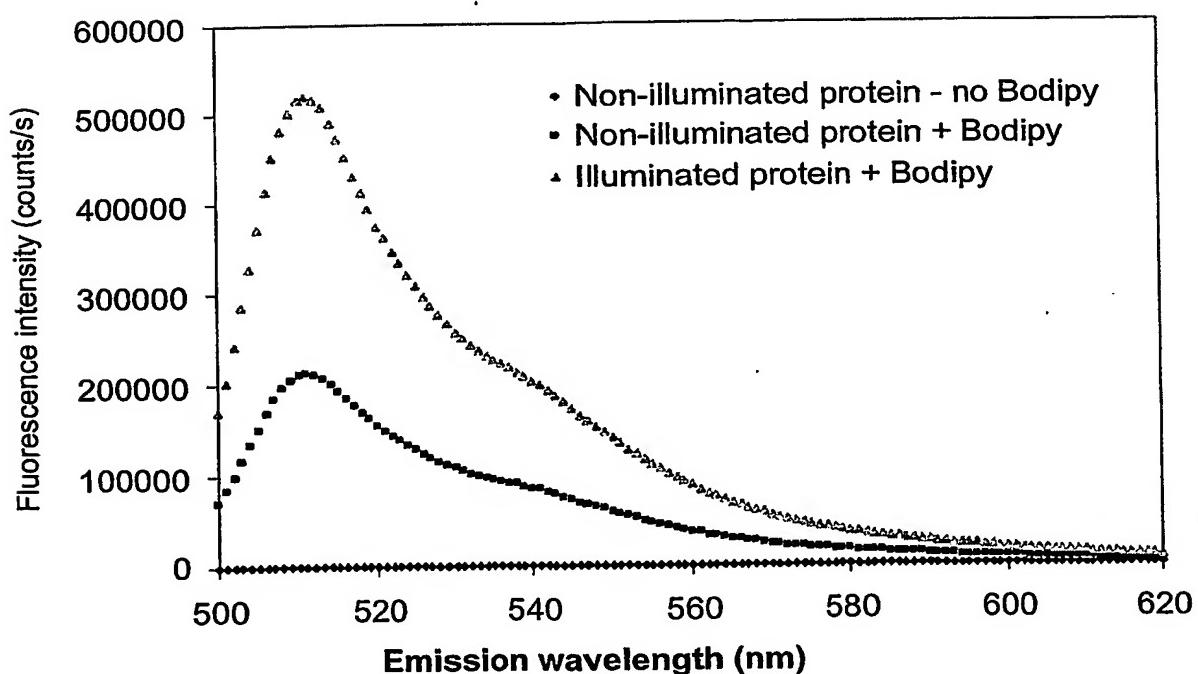
A**B****SUBSTITUTE SHEET (RULE 26)**

8/20

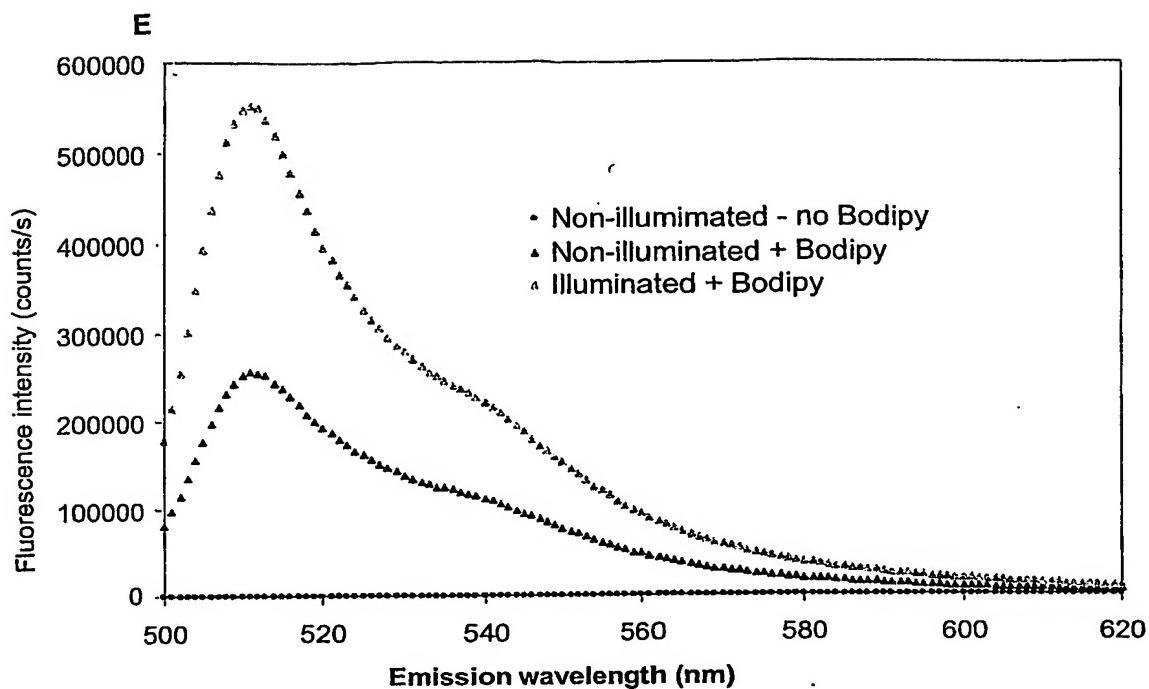
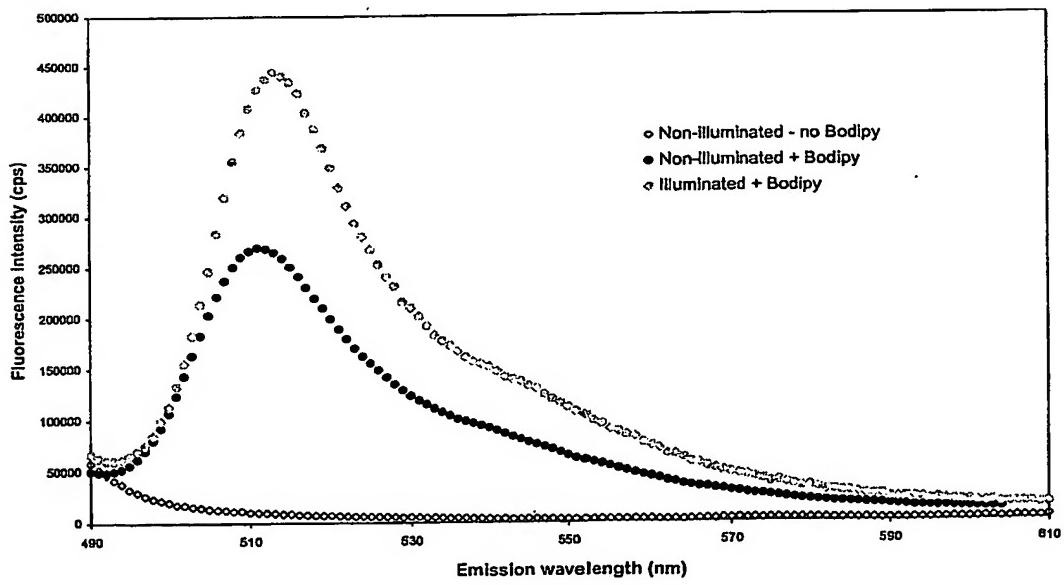
Figure 8

A**B**

9/20

C**D**

10/20

**F**

11/20

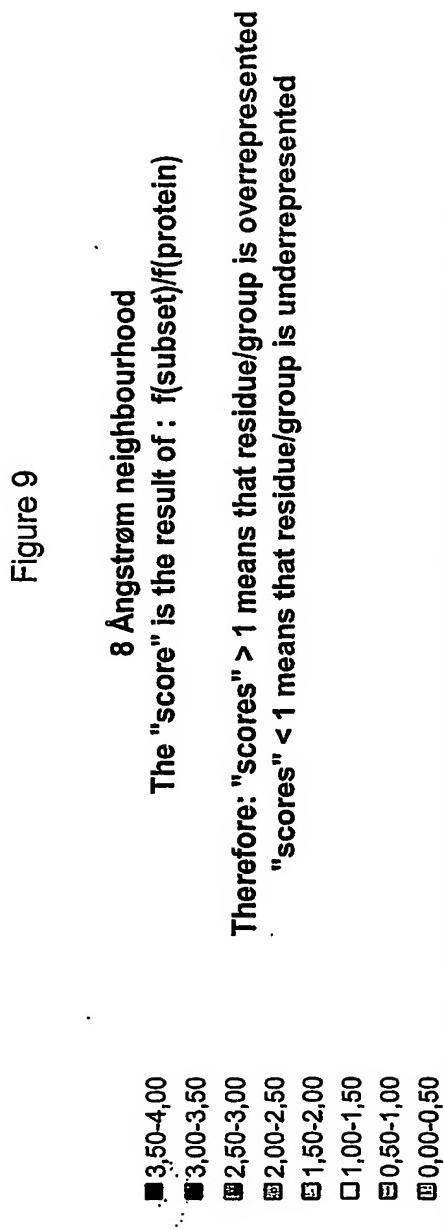
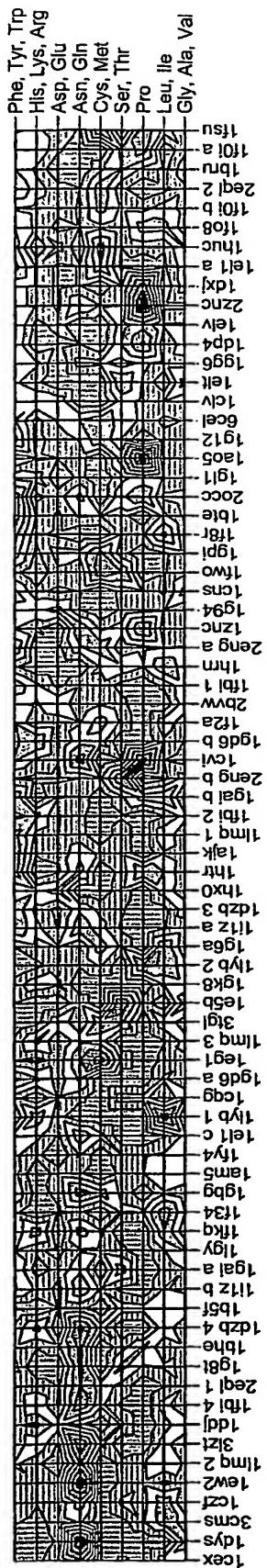


Figure 9

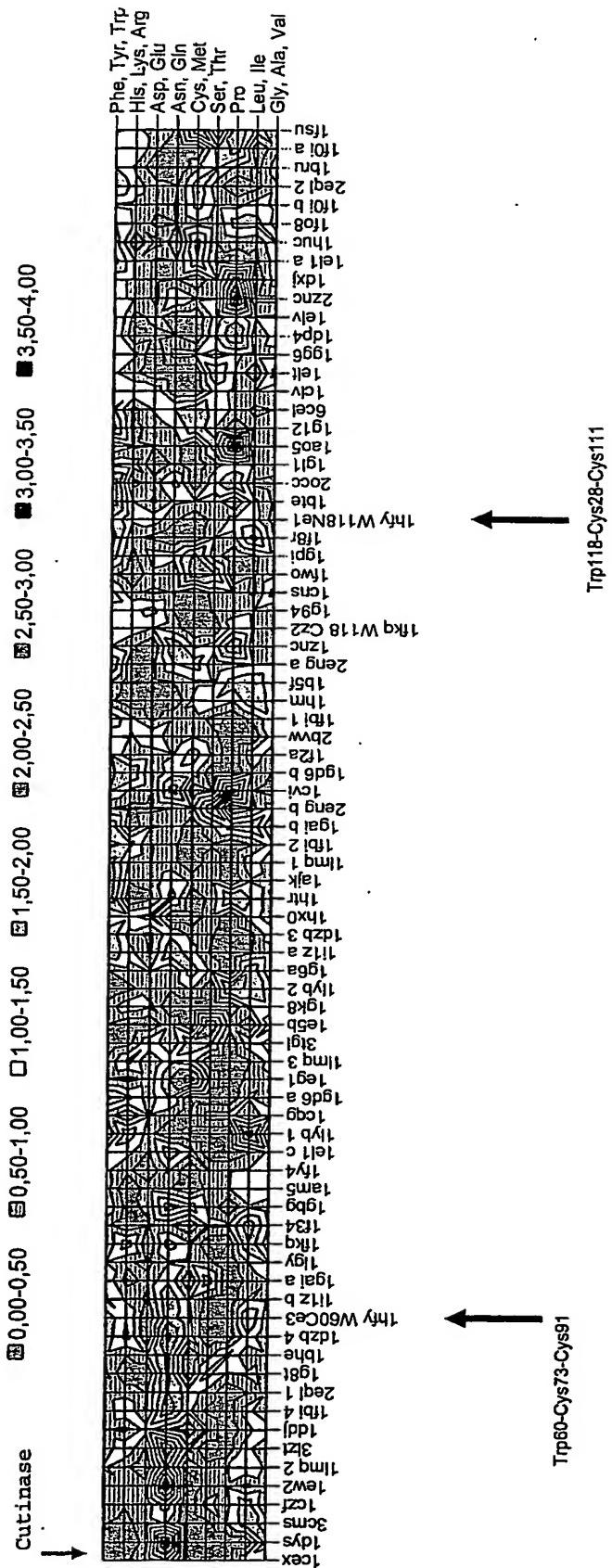


12/20

Figure 10

8 Ångström neighbourhood

Therefore: "scores" > 1 means that residue/group is overrepresented
"scores" < 1 means that residue/group is underrepresented



13/20

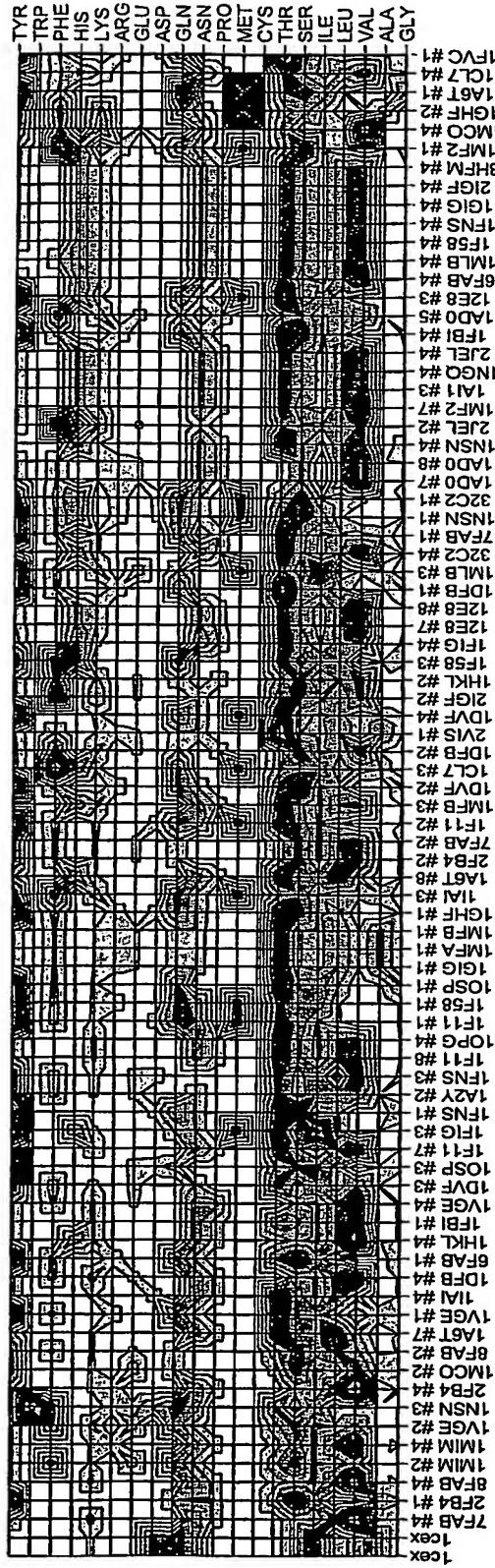
Figure 11

8 Ångström neighbourhood
The triad of cutinase compared to IGG1 triads A)

The "score" is the result of : $f(\text{subset})/f(\text{protein})$

Therefore: "scores" > 1 means that residue/group is overrepresented
 "scores" < 1 means that residue/group is underrepresented

0,00-0,50 ■ 0,50-1,00 ■ 1,00-1,50 ■ 1,50-2,00 ■ 2,00-2,50 ■ 2,50-3,00 ■ 3,00-3,50 ■ 3,50-4,00 ■ 4,00-4,50 ■ 4,50-5,00 ■ 5,00-5,50



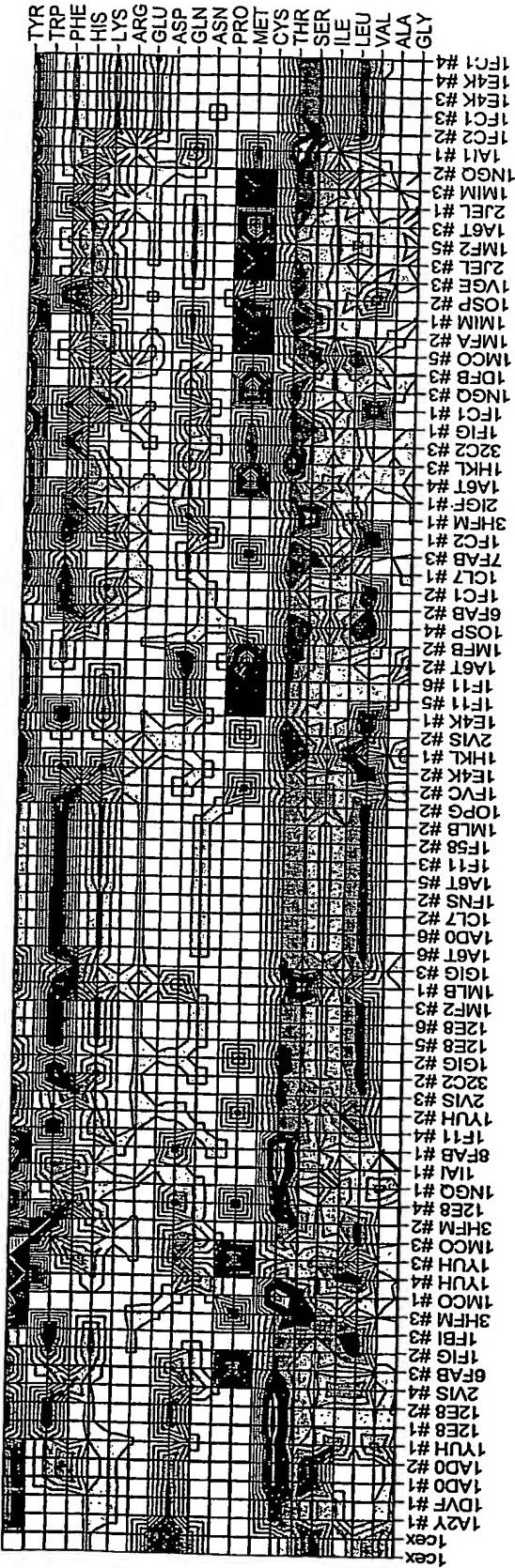
14/20

Figure 12

8 Ångstrøm neighbourhood
The triad of cutinase compared to IGG1 triads B)

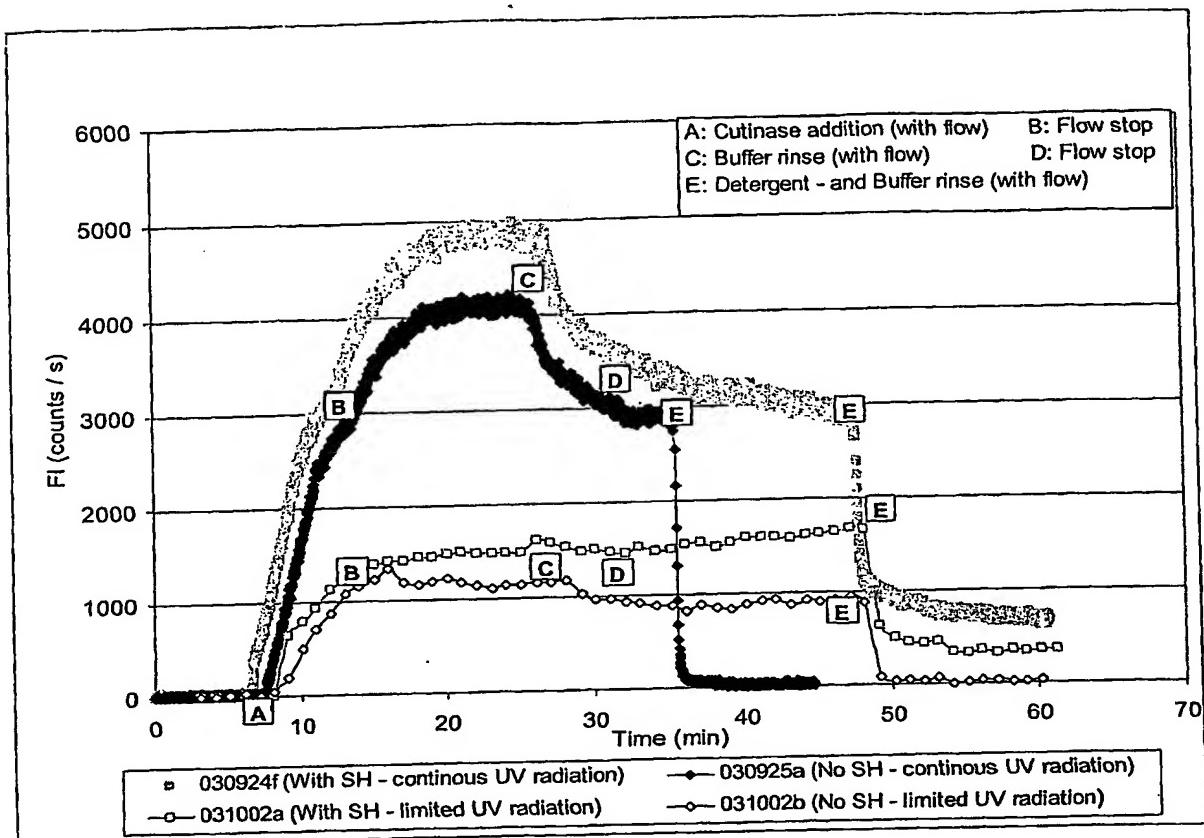
The "score" is the result of : $f(\text{subset})/f(\text{protein})$

Therefore: "scores" > 1 means that residue/group is overrepresented
 "scores" < 1 means that residue/group is underrepresented



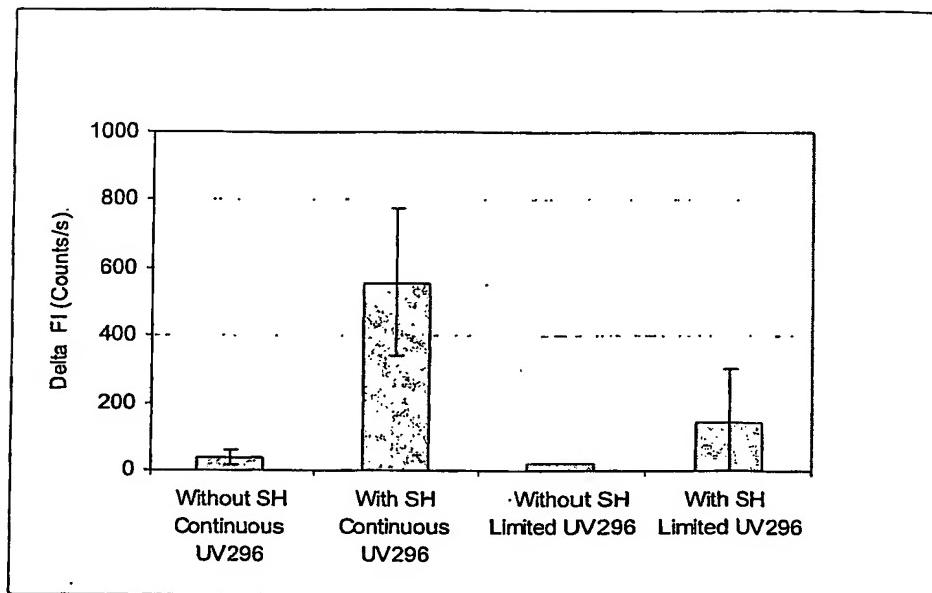
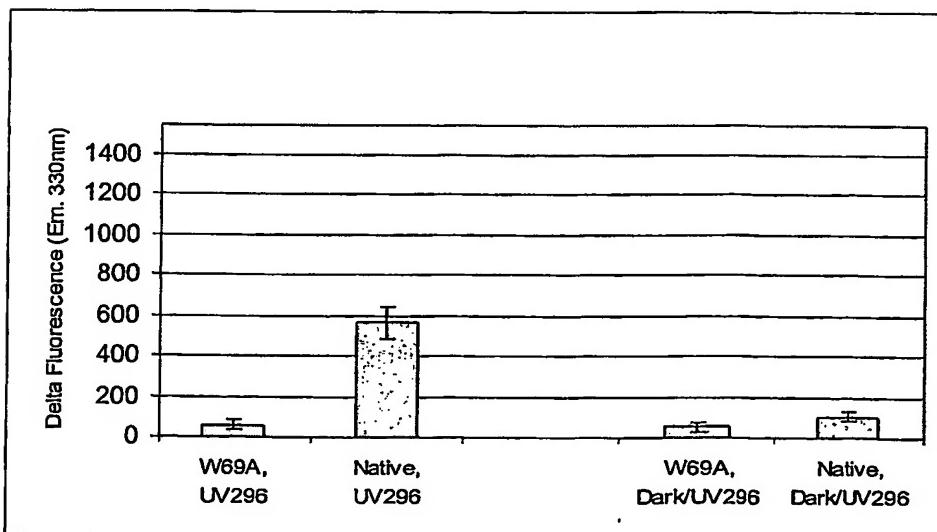
15/20

Figure 13



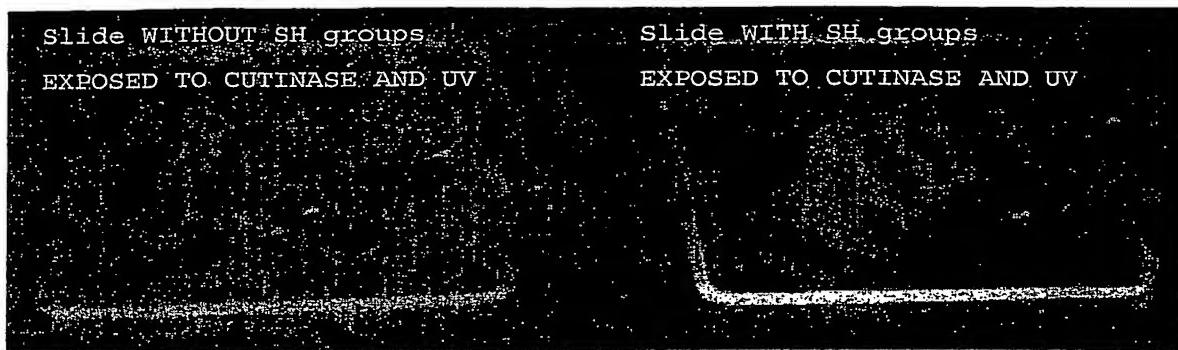
16/20

Figure 14

A**B**

17/20

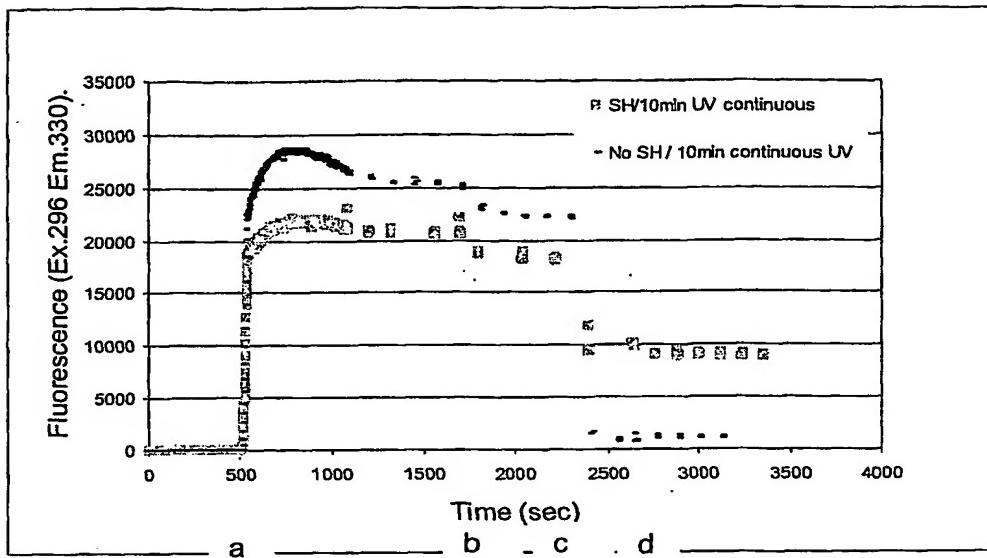
Figure 15



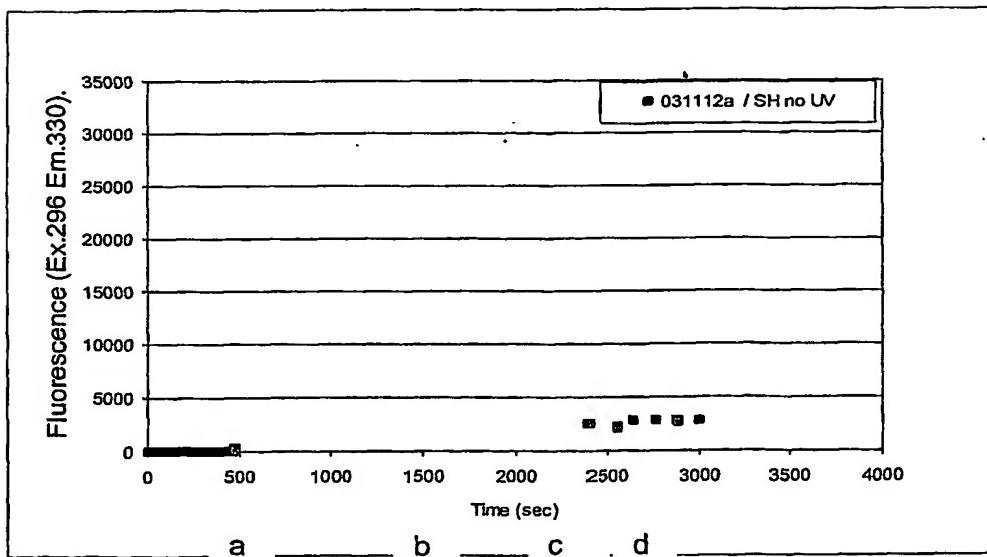
18/20

Figure 16

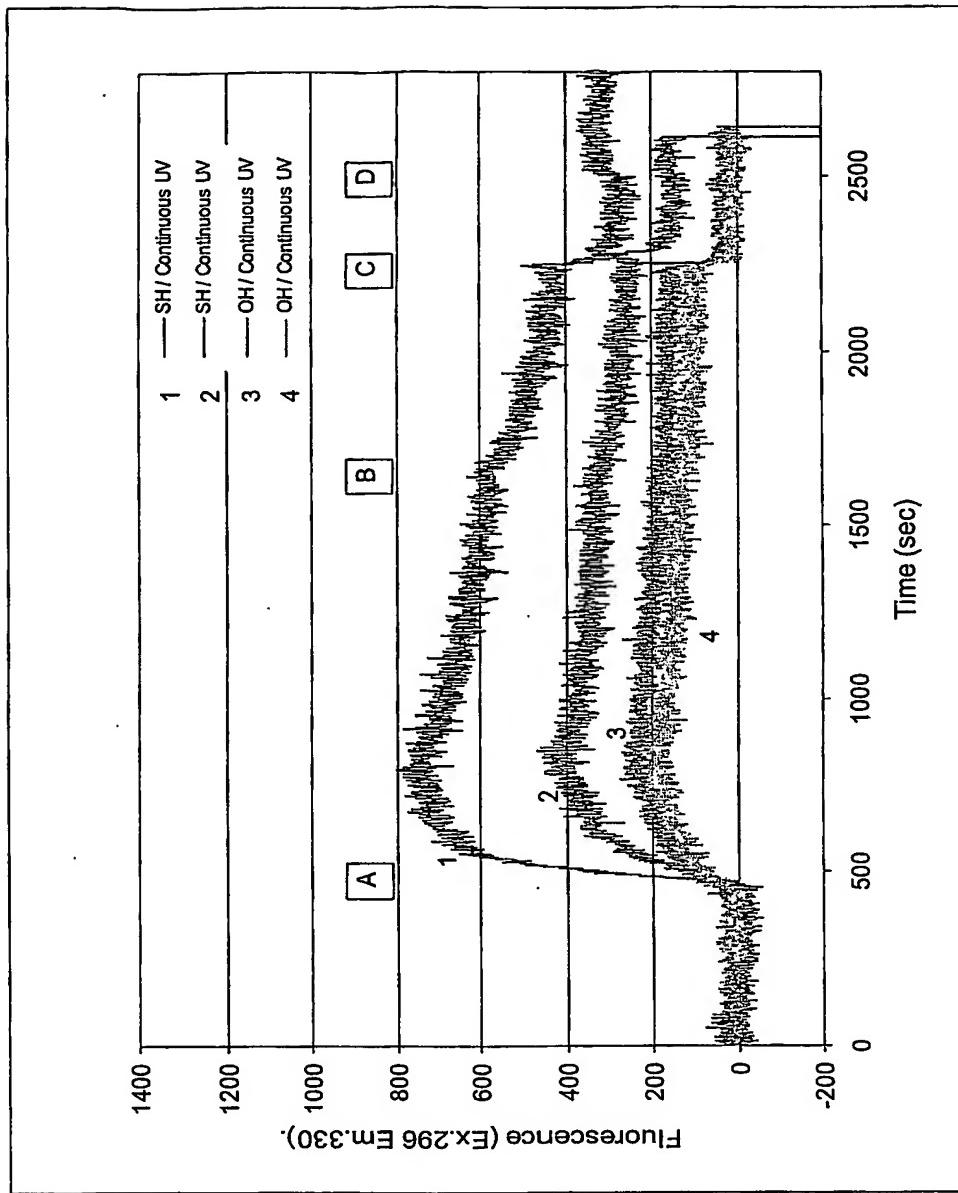
A



B



19/20



20/20

Figure 17 A

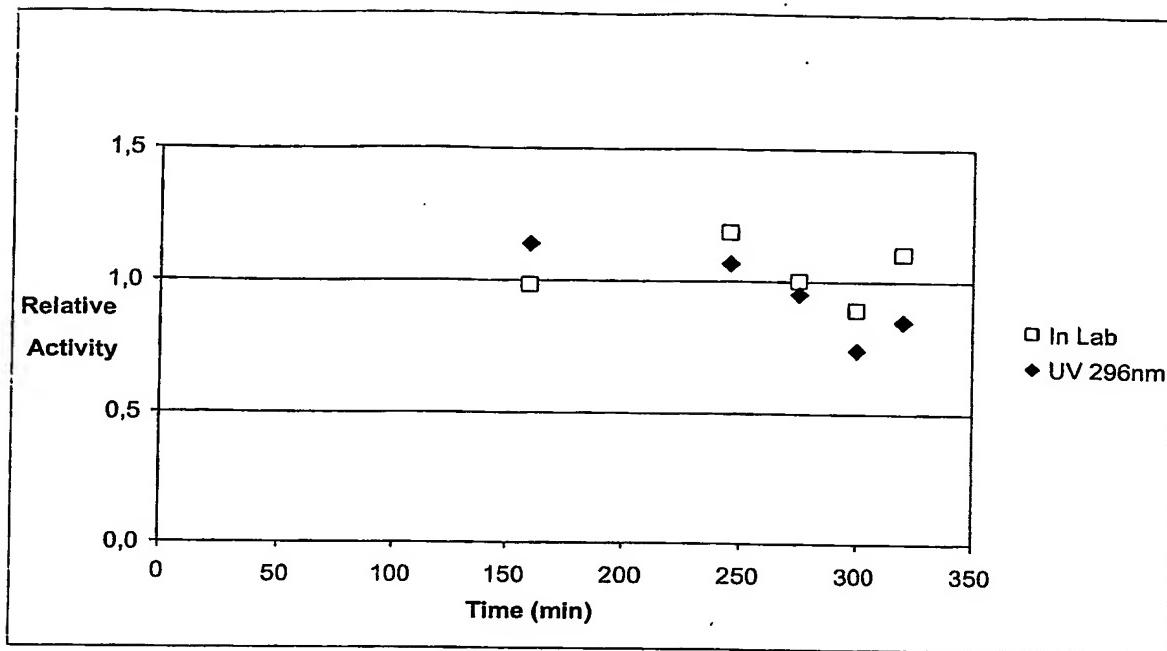


Figure 17B

